

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lal, Preeti
Corley, Neil C.
Patterson, Chandra
- (ii) TITLE OF THE INVENTION: HUMAN NEUROSECRETORY PROTEINS
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Dr.
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Cerrone, Michael C.
 - (B) REGISTRATION NUMBER: 39,132
 - (C) REFERENCE/DOCKET NUMBER: PF-0510 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-855-0555
 - (B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: ISLTNOT01
 - (B) CLONE: 2379427
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20070404 09:00:00

Met	Gly	Phe	Leu	Gly	Thr	Gly	Thr	Trp	Ile	Leu	Val	Leu	Val	Leu	Pro	1	5	10	15
Ile	Gln	Ala	Phe	Pro	Lys	Pro	Gly	Gly	Ser	Gln	Asp	Lys	Ser	Leu	His	20	25	30	
Asn	Arg	Glu	Leu	Ser	Ala	Glu	Arg	Pro	Leu	Asn	Glu	Gln	Ile	Ala	Glu	35	40	45	
Ala	Glu	Glu	Asp	Lys	Ile	Lys	Lys	Thr	Tyr	Pro	Pro	Glu	Asn	Lys	Pro	50	55	60	
Gly	Gln	Ser	Asn	Tyr	Ser	Phe	Val	Asp	Asn	Leu	Asn	Leu	Leu	Lys	Ala	65	70	75	80
Ile	Thr	Glu	Lys	Glu	Lys	Ile	Glu	Lys	Glu	Arg	Gln	Ser	Ile	Arg	Ser	85	90	95	
Ser	Pro	Leu	Asp	Asn	Lys	Leu	Asn	Val	Glu	Asp	Val	Asp	Ser	Thr	Lys	100	105	110	
Asn	Arg	Lys	Leu	Ile	Asp	Asp	Tyr	Asp	Ser	Thr	Lys	Ser	Gly	Leu	Asp	115	120	125	
His	Lys	Phe	Gln	Asp	Asp	Pro	Asp	Gly	Leu	His	Gln	Leu	Asp	Gly	Thr	130	135	140	
Pro	Leu	Thr	Ala	Glu	Asp	Ile	Val	His	Lys	Ile	Ala	Ala	Arg	Ile	Tyr	145	150	155	160
Glu	Glu	Asn	Asp	Arg	Ala	Val	Phe	Asp	Lys	Ile	Val	Ser	Lys	Leu	Leu	165	170	175	
Asn	Leu	Gly	Leu	Ile	Thr	Glu	Ser	Gln	Ala	His	Thr	Leu	Glu	Asp	Glu	180	185	190	
Val	Ala	Glu	Val	Leu	Gln	Lys	Leu	Ile	Ser	Lys	Glu	Ala	Asn	Asn	Tyr	195	200	205	
Glu	Glu	Asp	Pro	Asn	Lys	Pro	Thr	Ser	Trp	Thr	Glu	Asn	Gln	Ala	Gly	210	215	220	
Lys	Ile	Pro	Glu	Lys	Val	Thr	Pro	Met	Ala	Ala	Ile	Gln	Asp	Gly	Leu	225	230	235	240
Ala	Lys	Gly	Glu	Asn	Asp	Glu	Thr	Val	Ser	Asn	Thr	Leu	Thr	Leu	Thr	245	250	255	
Asn	Gly	Leu	Glu	Arg	Arg	Thr	Lys	Thr	Tyr	Ser	Glu	Asp	Asn	Phe	Glu	260	265	270	
Glu	Leu	Gln	Tyr	Phe	Pro	Asn	Phe	Tyr	Ala	Leu	Leu	Lys	Ser	Ile	Asp	275	280	285	
Ser	Glu	Lys	Glu	Ala	Lys	Glu	Lys	Glu	Thr	Leu	Ile	Thr	Ile	Met	Lys	290	295	300	
Thr	Leu	Ile	Asp	Phe	Val	Lys	Met	Met	Val	Lys	Tyr	Gly	Thr	Ile	Ser	305	310	315	320
Pro	Glu	Glu	Gly	Val	Ser	Tyr	Leu	Glu	Asn	Leu	Asp	Glu	Met	Ile	Ala	325	330	335	
Leu	Gln	Thr	Lys	Asn	Lys	Leu	Glu	Lys	Asn	Ala	Thr	Asp	Asn	Ile	Ser	340	345	350	
Lys	Leu	Phe	Pro	Ala	Pro	Ser	Glu	Lys	Ser	His	Glu	Glu	Thr	Asp	Ser	355	360	365	
Thr	Lys	Glu	Glu	Ala	Ala	Lys	Met	Glu	Lys	Glu	Tyr	Gly	Ser	Leu	Lys	370	375	380	
Asp	Ser	Thr	Lys	Asp	Asp	Asn	Ser	Asn	Pro	Gly	Gly	Lys	Thr	Asp	Glu	385	390	395	400
Pro	Lys	Gly	Lys	Thr	Glu	Ala	Tyr	Leu	Glu	Ala	Ile	Arg	Lys	Asn	Ile	405	410	415	
Glu	Trp	Leu	Lys	Lys	His	Asp	Lys	Lys	Gly	Asn	Lys	Glu	Asp	Tyr	Asp	420	425	430	
Leu	Ser	Lys	Met	Arg	Asp	Phe	Ile	Asn	Lys	Gln	Ala	Asp	Ala	Tyr	Val	435	440	445	
Glu	Lys	Gly	Ile	Leu	Asp	Lys	Glu	Glu	Ala	Glu	Ala	Ile	Lys	Arg	Ile	450	455	460	

Tyr Ser Ser Leu
465

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ISLTNOT01
- (B) CLONE: 2379427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGCGCTCCC	CTCTACCTGG	AGACTTGACT	CCCGCGCGCC	CCAACCCTGC	TTATCCCTTG	60
ACCGTCGAGT	GTCAGAGATC	CTGCAGCCGC	CCAGTCCCGG	CCCCTCTCCC	GCCCCACACC	120
CACCCTCCTG	GCTCTTCCTG	TTTTTACTCC	TCCTTTTCAT	TCATAACAAA	AGCTACAGCT	180
CCAGGAGCCC	AGCGCCGGGC	TGTGACCCAA	GCCGAGCGTG	GAAGAATGGG	GTTCTCTCGG	240
ACCGGCACCT	GGATTCTGGT	GTTAGTGCTC	CCGATTCAAG	CTTTCCCCAA	ACCTGGAGGA	300
AGCCAAGACA	AATCTCTACA	TAATAGAGAA	TTAAGTGCAG	AAAGACCTTT	GAATGAACAG	360
ATTGCTGAAG	CAGAAGAAGA	CAAGATTAAA	AAAACATATC	CTCCAGAAAA	CAAGCCAGGT	420
CAGAGCAACT	ATTCTTTTGT	TGATAACTTG	AACCTGCTAA	AGGCAATAAC	AGAAAAGGAA	480
AAAATTGAGA	AAGAAAGACA	ATCTATAAGA	AGCTCCCCAC	TTGATAATAA	GTTGAATGTG	540
GAAGATGTTG	ATTCAACCAA	GAATCGAAAA	CTGATCGATG	ATTATGACTC	TACTAAGAGT	600
GGATTGGATC	ATAAATTTCA	AGATGATCCA	GATGGTCTTC	ATCAACTAGA	CGGGACTCCT	660
TTAACCGCTG	AAGACATTGT	CCATAAAATC	GCTGCCAGGA	TTTATGAAGA	AAATGACAGA	720
GCCGTGTTTG	ACAAGATTGT	TTCTAAACTA	CTTAATCTCG	GCCTTATCAC	AGAAAGCCAA	780
GCACATACAC	TGGAAGATGA	AGTAGCAGAG	GTTTTACAAA	AATTAATCTC	AAAGGAAGCC	840
AACAATTATG	AGGAGGATCC	CAATAAGCCC	ACAAGCTGGA	CTGAGAATCA	GGCTGGAAAA	900
ATACCAGAGA	AAGTGACTCC	AATGGCAGCA	ATTCAAGATG	GTCTTGCTAA	GGGAGAAAAC	960
GATGAAACAG	TATCTAACAC	ATTAACCTTG	ACAAATGGCT	TGGAAAGGAG	AACTAAAACC	1020
TACAGTGAAG	ACAACCTTGA	GGAACCTCAA	TATTTCCCAA	ATTTCTATGC	GCTACTGAAA	1080
AGTATTGATT	CAGAAAAAGA	AGCAAAAGAG	AAAGAAACAC	TGATTACTAT	CATGAAAACA	1140
CTGATTGACT	TTGTGAAGAT	GATGGTGAAA	TATGGAACAA	TATCTCCAGA	AGAAGGTGTT	1200
TCCTACCTTG	AAAACCTTGA	TGAAATGATT	GCTCTTCAGA	CCAAAAACAA	GCTAGAAAAA	1260
AATGCTACTG	ACAATATAAG	CAAGCTTTTC	CCAGCACCAT	CAGAGAAGAG	TCATGAAGAA	1320
ACAGACAGTA	CCAAGGAAGA	AGCAGCTAAG	ATGGAAAAGG	AATATGGAAG	CTTGAAGGAT	1380
TCCACAAAAG	ATGATAACTC	CAACCCAGGA	GGAAAGACAG	ATGAACCCAA	AGGAAAAACA	1440
GAAGCCTATT	TGGAAGCCAT	CAGAAAAAAT	ATTGAATGGT	TGAAGAAACA	TGACAAAAAG	1500
GGAAATAAAG	AAGATTATGA	CCTTTCAAAG	ATGAGAGACT	TCATCAATAA	ACAAGCTGAT	1560
GCTTATGTGG	AGAAAGGCAT	CCTTGACAAG	GAAGAAGCCG	AGGCCATCAA	GCGCATTAT	1620
AGCAGCCTGT	AAAAATGGCA	AAAGATCCAG	GAGTCTTTCA	ACTGTTTCAG	AAAACATAAT	1680
ATAGCTTAAA	ACACTTCTAA	TTCTGTGATT	AAAATTTTTT	GACCCAAGGG	TTATTAGAAA	1740
GTGCTGAATT	TACAGTAGTT	AACCTTTTAC	AAGTGGTTAA	AACATAGCTT	TCTTCCCGTA	1800
AAAACATATCT	GAAAGTAAAG	TTGTATGTAA	GCTGAAAAAA	AAAA		1844

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT14

PF-0510 US

(B) CLONE: 2744187

2013 04 20 00 00 00

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala Ala
 1 5 10 15
 Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser
 20 25 30
 Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro
 35 40 45
 Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu
 50 55 60
 Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro
 65 70 75 80
 Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser
 85 90 95
 Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr
 100 105 110
 Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr
 115 120 125
 Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe Asp Pro
 130 135 140
 Ser Lys Ile Gln Leu Pro Glu Asp Glu
 145 150

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT14
 (B) CLONE: 2744187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGCCGCTGG CTCCGTTTCA CTTCCCAGCC ACCCCCGCTG CTGCTACCAT GATCTGCCAG 60
 CCTGGGTGAT GCTTCCTGCA GGGACTCTTC TCGGCCCGGG CTGTCAAGGA AGGGCTCCCA 120
 GACATCACCT CTGCCGCGC CCACCTCCTC CAACTCTCCC AGCTCAGCCG GAGCCGGAGC 180
 GCGCAACAAC CAAGTCCGAG ACTGGAGGCA GATCGGGGGG AGGGGAGAAG CGCCAAGCGC 240
 GCTGCCCTCC CAGGGAAACT CACTGCCGCC TACTCCCAGC CGGCCACAGT CACCAGCTCA 300
 AAATGGCGAC GACGAGAAGG GAGTCGGCGC TCCGACCACC ATCCACCTAC TAAGGAAGCG 360
 CGCTCTGGCC GGCCCCGGCG ATTGGTCACC GCCCGCTAGG GGACAGCCCT GGCCTCCTCT 420
 GATTGGCAAG CGCTGGCCAC CTCCCCACAC CCCTTGCGAA CGCTCCCCTA GTGGAGAAAA 480
 GGAGTAGCTA TTAGCCAATT CGGGCAGGGC CCGCTTTTTA GAAGCTTGAT TTCCTTTGAA 540
 GATGAAAGAC TAGCGGAAGC TCTGCCTCTT TCCCCAGTGG GCGAGGGAAC TCGGGGCGAT 600
 TGGCTGGGAA CTGTATCCAC CAAATGTCAC CGATTCTTCC TATGCAGGAA ATGAGCAGAC 660
 CCATCAATAA GAAATTTCTC AGCCTGGCCG AAAATGGTTG GCCCCACGAA GCCACGACAA 720
 CTGGAGGCAA AGAGGGTTGC TCAACGCCCC GCCTCATTGG AAAACCAAAT CAGATCTGGG 780
 ACCTATATAG CGTGGCGGAG GCGGGGCGAT GATTGTCGCG CTCGCACCCA CTGCAGCTGC 840
 GCACAGTCGC ATTTCTTTCC CCGCCCCCTGA GACCCTGCAG CACCATCTGT CATGGCGGCT 900
 GGGCTGTTTG GTTTGAGCGC TCGCCGTCTT TTGGCGGCAG CGGCGACGCG AGGGCTCCCC 960
 GCCGCCCGCG TCCGCTGGGA ATCTAGCTTC TCCAGGACTG TGGTCGCCCC GTCCGCTGTG 1020
 GCGGGAAGC GGCCCCCAGA ACCGACCACA CCGTGGCAAG AGGACCCAGA ACCCGAGGAC 1080
 GAAACTTGT ATGAGAAGAA CCCAGACTCC CATGGTTATG ACAAGGACCC CGTTTGGAC 1140
 GTCTGGAACA TGCGACTTGT CTTCTTCTTT GGCGTCTCCA TCATCCTGGT CCTTGGCAGC 1200
 ACCTTTGTGG CCTATCTGCC TGACTACAGG ATGAAAGAGT GGTCCCGCCG CGAAGCTGAG 1260

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AGGCTTGTGA AATACCGAGA GGCCAATGGC CTTCCCATCA TGGAATCCAA CTGCTTCGAC 1320
CCCAGCAAGA TCCAGCTGCC AGAGGATGAG TGACCAGTTG CTAAGTGGGG CTCAAGAAGC 1380
ACCGCCTTCC CCACCCCCTG CCTGCCATTC TGACCTCTTC TCAGAGCACC TAATTAAAGG 1440
GGCTGAAAGT CTGAAAAAAA AAA 1463

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 413764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Gly Phe Leu Trp Thr Gly Ser Trp Ile Leu Val Leu Val Leu Asn
 1           5           10           15
Ser Gly Pro Ile Gln Ala Phe Pro Lys Pro Glu Gly Ser Gln Asp Lys
          20           25           30
Ser Leu His Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln
          35           40           45
Ile Ala Glu Ala Glu Ala Asp Lys Ile Lys Lys Ala Phe Pro Ser Glu
          50           55           60
Ser Lys Pro Ser Glu Ser Asn Tyr Ser Ser Val Asp Asn Leu Asn Leu
          65           70           75           80
Leu Arg Ala Ile Thr Glu Lys Glu Thr Val Glu Lys Glu Arg Gln Ser
          85           90           95
Ile Arg Ser Pro Pro Phe Asp Asn Gln Leu Asn Val Glu Asp Ala Asp
          100          105          110
Ser Thr Lys Asn Arg Lys Leu Ile Asp Glu Tyr Asp Ser Thr Lys Ser
          115          120          125
Gly Leu Asp His Lys Phe Gln Asp Asp Pro Asp Gly Leu His Gln Leu
          130          135          140
Asp Gly Thr Pro Leu Thr Ala Glu Asp Ile Val His Lys Ile Ala Thr
          145          150          155          160
Arg Ile Tyr Glu Glu Asn Asp Arg Gly Val Phe Asp Lys Ile Val Ser
          165          170          175
Lys Leu Leu Asn Leu Gly Leu Ile Thr Glu Ser Gln Ala His Thr Leu
          180          185          190
Glu Asp Glu Val Ala Glu Ala Leu Gln Lys Leu Ile Ser Lys Glu Ala
          195          200          205
Asn Asn Tyr Glu Glu Thr Leu Asp Lys Pro Thr Ser Arg Thr Glu Asn
          210          215          220
Gln Asp Gly Lys Ile Pro Glu Lys Val Thr Pro Val Ala Ala Val Gln
          225          230          235          240
Asp Gly Phe Thr Asn Arg Glu Asn Asp Glu Thr Val Ser Asn Thr Leu
          245          250          255
Thr Leu Ser Asn Gly Leu Glu Arg Arg Thr Asn Pro His Arg Glu Asp
          260          265          270
Asp Phe Glu Glu Leu Gln Tyr Phe Pro Asn Phe Tyr Ala Leu Leu Thr
          275          280          285
Ser Ile Asp Ser Glu Lys Glu Ala Lys Glu Lys Glu Thr Leu Ile Thr
          290          295          300
Ile Met Lys Thr Leu Ile Asp Phe Val Lys Met Met Val Lys Tyr Gly
          305          310          315          320

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Thr Ile Ser Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn Leu Asp Glu
      325                      330                      335
Thr Ile Ala Leu Gln Thr Lys Asn Lys Leu Glu Lys Asn Thr Thr Asp
      340                      345                      350
Ser Lys Ser Lys Leu Phe Pro Ala Pro Pro Glu Lys Ser Gln Glu Glu
      355                      360                      365
Thr Asp Ser Thr Lys Glu Glu Ala Ala Lys Met Glu Lys Glu Tyr Gly
      370                      375                      380
Ser Leu Lys Asp Ser Thr Lys Asp Asp Asn Ser Asn Leu Gly Gly Lys
      385                      390                      395                      400
Thr Asp Glu Ala Thr Gly Lys Thr Glu Ala Tyr Leu Glu Ala Ile Arg
      405                      410                      415
Lys Asn Ile Glu Trp Leu Lys Lys His Asn Lys Lys Gly Asn Lys Glu
      420                      425                      430
Asp Tyr Asp Leu Ser Lys Met Arg Asp Phe Ile Asn Gln Gln Ala Asp
      435                      440                      445
Ala Tyr Val Glu Lys Gly Ile Leu Asp Lys Glu Glu Ala Asn Ala Ile
      450                      455                      460
Lys Arg Ile Tyr Ser Ser Leu
      465                      470

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1771306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser Arg Ala
  1                      5                      10                      15
Val Ile Ala Pro Ser Gly Val Glu Lys Lys Arg Gln Arg Glu Pro Thr
      20                      25                      30
Met Gln Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu Asn Val Tyr Ala
      35                      40                      45
Lys Asn Pro Asp Phe His Gly Tyr Asp Ser Asp Pro Val Val Asp Val
      50                      55                      60
Trp Asn Met Arg Ala Val Phe Phe Phe Gly Phe Ser Ile Val Leu Val
      65                      70                      75                      80
Phe Gly Thr Thr Phe Val Ala Tyr Val Pro Asp Tyr Arg Met Gln Glu
      85                      90                      95
Trp Ala Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Val Asn
      100                      105                      110
Gly Leu Pro Ile Met Glu Ser Asn Tyr Phe Asp Pro Ser Lys Ile Gln
      115                      120                      125
Leu Pro Glu Asp Asp
      130

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